Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for identifying an inhibitor compounds capable of reducing the interaction between a first region and a second region, comprising:

a) placing in contact:

i) a potential inhibitor compound;

ii) a first region which is a fragment of ~~signature motif on~~ a nuclear protein, wherein the fragment comprises a signature motif B^1XXLL, in which B^1 is any natural hydrophobic amino acid, L is leucine, and X independently represents any natural amino acid, and the signature motif is a structural element of a nuclear protein that binds to a liganded nuclear receptor in the process of activating or repressing target genes, and the nuclear protein is a bridging factor responsible for an interaction between a liganded nuclear receptor transcription factor and a transcription initiation complex involved in regulation of gene expression; provided that a fragment that includes residues 624-1287 of TIF-2 is excluded;

[b)] iii) a second region which is a liganded nuclear receptor transcription factor or a fragment thereof, wherein the fragment comprises that part of the ~~a~~ nuclear receptor which is capable of interacting with the nuclear protein through binding to the signature motif; [,]and

~~wherein:~~

~~the nuclear protein is a bridging factor that is responsible for the interaction between a liganded nuclear receptor and a transcription initiation complex involved in regulation of gene expression;~~

~~the nuclear receptor is a transcription factor;~~

~~the signature motif is a short sequence of amino acid residues which is the key structural element of a nuclear protein which binds to a liganded nuclear receptor as part of the process of the activation or repression of target genes; and~~

~~in which the method comprises taking:~~

~~i) the potential inhibitor compound;~~

~~ii) the liganded nuclear receptor or a fragment thereof in which the fragment comprises the second region defined in this claim in b) above;~~

~~iii) a fragment comprising a signature motif of the nuclear protein; and~~

~~iv) detecting the presence or absence of inhibition of theinteraction between ii) and iii).~~

b) detecting the presence or absence of inhibition of the interaction between ii) and iii).

2. (Cancelled)

3. (Currently Amended) A method according to claim 23 ~~2 or claim 5~~, wherein ~~in which~~ B^1 is leucine or valine.

4. (Currently Amended) A method according to claim 3, wherein ~~in which~~ B^1 is leucine.

5. (Withdrawn - Currently Amended) A method according to claims 1, 3, 4, or 23 wherein ~~in which~~ the signature motif is B^2B^1XXLL wherein B^2 is a~~ny natural~~ hydrophobic amino acid~~, B^2 is a hydrophobic amino acid, L is leucine and X independently represents any natural amino acid~~.

6. (Withdrawn - Currently Amended) A method according to claim 5, wherein ~~in which~~ B^2 is selected from ~~the group consisting of~~ isoleucine, leucine, methionine, phenylalanine, tryptophan, tyrosine and valine.

7. (Currently Amended) A method according to ~~any one of~~ claims 1, 3, 4, or 23 ~~2 and 5~~, wherein ~~in which~~ the nuclear protein is a coactivator.

8. (Currently Amended) A method according to claim 7, wherein [~~in which~~] the coactivator is selected from ~~the group consisting of~~ RIP 140, SRC-1, TIF2, CBP, p300, TIF1, Trip1, Trip2, Trip3, Trip4, Trip5, Trip8, Trip9, p/CIP, ARA70 & Trip230.

9. (Currently Amended) A method according to ~~any one of~~ claims 1, 3, 4, or 23 ~~2 and 5~~, wherein ~~in which~~ the transcription factor is a steroid hormone receptor.

10. (Currently Amended) A method according to claim 9, wherein ~~in which~~ the steroid hormone receptor is selected from ~~the group consisting of~~ oestrogen receptor, progesterone receptor, androgen receptor and glucocorticoid receptor.

11. (Currently Amended) A method according to claim 10, wherein ~~in which~~ the steroid hormone receptor is oestrogen receptor.

12. (Currently Amended) A method according to ~~any one of~~ claims 1, 3, 4, or 23 ~~and 5~~, wherein the method is ~~in the form of~~ a 2-hybrid assay ~~system~~.

13. (Currently Amended) A method according to ~~any one of~~ claims 1, 3, 4, or 23 ~~2 and 5~~, wherein the potential inhibitor compound is a member ~~in the form~~ of a peptide library based on the ~~a~~ signature motif ~~as defined in said claim~~.

14. (Withdrawn) A novel inhibitor identified according to the method defined in any one of claims 1, 2 and 5 which reduces the interaction between

a) a first region which is a signature motif on a nuclear protein, and

b) a second region which is that part of a nuclear receptor which is capable of interacting with the nuclear protein through binding to the signature motif, wherein:

the nuclear protein is a bridging factor that is responsible for the interaction between a liganded nuclear receptor and the transcription initiation complex involved in regulation of gene expression;

the nuclear receptor is a transcription factor;

the signature motif is a short sequence of amino acid residues which is the key structural element of a nuclear protein which binds to the liganded nuclear receptor as part of the process of activation or repression of target genes.

15. (Withdrawn) An inhibitor according to claim 14 which is a peptide of less than 15 amino acid residues.

16. (Withdrawn) An inhibitor according to claim 15 selected from the group consisting of PQAQQKSLLQQLLT (SEQ ID NO: 2), KLVQLLTTT (SEQ ID NO: 3), ILHRLLQE (SEQ ID NO: 4) and LLQQLLTE (SEQ ID NO:5).

17. (Withdrawn) An inhibitor according to claim 14 comprising an antibody which specifically binds to a signature motif on a nuclear protein.

18. (Withdrawn) A pharmaceutical composition which comprises an inhibitor as defined in claim 14 or a pharmaceutically-acceptable salt thereof, in association with a pharmaceutically-acceptable diluent or carrier.

19. (Withdrawn) A method of mapping nuclear receptor interaction domains in nuclear proteins in which the method comprises analysis of the sequence of a nuclear protein for the presence of signature motifs as defined in any one of claims 1, 2 and 5 in order to identify an interaction domain or a potential interaction domain.

20. (Withdrawn) A pharmaceutical composition which comprises an inhibitor as defined in claim 15 or a pharmaceutically-acceptable salt thereof, in association with a pharmaceutically-acceptable diluent or carrier.

21. (Withdrawn) A pharmaceutical composition which comprises an inhibitor as defined in claim 16 or a pharmaceutically-acceptable salt thereof, in association with a pharmaceutically-acceptable diluent or carrier.

22. (Withdrawn) A pharmaceutical composition which comprises an inhibitor as defined in claim 17 or a pharmaceutically-acceptable salt thereof, in association with a pharmaceutically-acceptable diluent or carrier.

23. (New) A method according to claim 1, wherein the fragment of a nuclear protein comprises only one signature motif.

Applicant believes no fee is due with this response. However, if a fee is due, please charge our Deposit Account No. 18-1945, under Order No. ASZD-P01-228 from which the undersigned is authorized to draw.

Dated: March 25, 2005

Respectfully submitted,

By _____

Weishi Li, Ph.D.
Registration No.: 53,217
ROPES & GRAY LLP
One International Place
Boston, Massachusetts 02110-2624
(617) 951-7000
(617) 951-7050 (Fax)
Attorneys/Agents For Applicant